



Blast 2 Sequences results

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BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.5 [Nov-16-2002]

Match: Mismatch: gap open: gap extension:
x_dropoff: expect: wordsize: Filter Align

Sequence 1 gi_1271750 yz97c02.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:290978 5' similar to PIR:S01302 S01302 hypothetical protein, 58K ;

Length 386 (1 .. 386)

Sequence 2 gi_16588686

Length 2677 (1 .. 2677)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 694 bits (361), Expect = 0.0
Identities = 383/387 (98%), Gaps = 3/387 (0%)
Strand = Plus / Plus



Query: 1 tccaaagctggaaan-tctgtgttccggccatgaacgtcaatgattctgttaccaaacag 59

Sbjct: 1164 tccaaagctggaaagctctgtgttccggccatgaacgtcaatgattctgttaccaaacag 1223

S-adenosylhomocysteine hydrolas> 266 S K A G K L C V P A M N V N D S V T K Q

Query: 60 aagtttgataacttgtactgctgccgagaatccatttggatggcctaaggaccaca 119

Sbjct: 1224 aagtttgataacttgtactgctgccgagaatccatttggatggcctaaggaccaca 1283

S-adenosylhomocysteine hydrolas> 286 K F D N L Y C C R E S I L D G L K R T T

Query: 120 gatgtgatgttggaaacaacaagtgggtgtggctatggtaggtaggcaaggc 179

Sbjct: 1284 gatgtgatgttggaaacaacaagtgggtgtggctatggtaggtaggcaaggc 1343

S-adenosylhomocysteine hydrolas> 306 D V M F G G K Q V V V C G Y G E V G K G

Query: 180 tgctgtgctctcaaagcttggagcaattgtctacattaccgaaatcgaccccac 239

Sbjct: 1344 tgctgtgctctcaaagcttggagcaattgtctacattaccgaaatcgaccccac 1403

S-adenosylhomocysteine hydrolas> 326 C C A A L K A L G A I V Y I T E I D P I

Query: 240 tgtgctctgcaggcctgcatggatgggtcaggggtggtaaagctaaatgaagtcatccg 299

Sbjct: 1404 tgtgctctgcaggcctgcatggatgggtcaggggtggtaaagctaaatgaagtcatccg 1463

S-adenosylhomocysteine hydrolas> 346 C A L Q A C M D G F R V V K L N E V , I R

Query: 300 caagtcgtgtcgtaataacttngcacagggaaaataagaatgttagtgcacacggngagcact 359

Sbjct: 1464 caagtcgtgtcgtaataacttngcacagggaaaataagaatgttagtgcacacggngagcact 1523

Sbjct: 1464 caagtcgatgtcgtaataactt-gcacaggaaataagaatgttagtgacacgg-gagcact 1521
S-adenosylhomocysteine hydrolas> 366 Q V D V V I T C T G N K N V V T R E H

Query: 360 tggatcgcataaaaacagtttatcg 386

|||||||
Sbjct: 1522 tggatcgcataaaaacagtttatcg 1548
S-adenosylhomocysteine hydrolas> 385 L D R M K N S C I

CPU time: 0.06 user secs. 0.05 sys. secs 0.11 total secs.

Lambda K H
1.33 0.621 1.12

Gapped
Lambda K H
1.33 0.621 1.12

Matrix: blastn matrix:1 -2

Gap Penalties: Existence: 5, Extension: 2

Number of Hits to DB: 6

Number of Sequences: 0

Number of extensions: 6

Number of successful extensions: 4

Number of sequences better than 10.0: 1

Number of HSP's better than 10.0 without gapping: 1

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 1

length of query: 386

length of database: 8,484,804,551

effective HSP length: 24

effective length of query: 362

effective length of database: 8,484,804,527

effective search space: 3071499238774

effective search space used: 3071499238774

T: 0

A: 0

X1: 6 (11.5 bits)

X2: 26 (50.0 bits)

S1: 12 (23.8 bits)

S2: 20 (39.1 bits)